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Department of War Influenza Surveillance and Mid-Season Vaccine Effectiveness

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Briefing Outline

- Purpose: To provide an update to on DoW influenza surveillance activities for 2025–2026
  - Program Descriptions
  - Vaccine Effectiveness in DoW Populations
    - ✓ DoW Beneficiaries
    - ✓ DoW Active Component Service members
  - DoW Phylogenetic Analyses
  - DoW Antigenic Characterization

Influenza Surveillance in the DoW: Overview

- **Global Influenza Surveillance**
  - Approximately 400 locations in over 30 countries
    - ✓ Military, local government/academic
  - Extensive characterization capabilities within the DoW
    - ✓ Culture, PCR, sequencing, serology
  - Rapid sharing of results with CDC and/or regional WHO reference centers

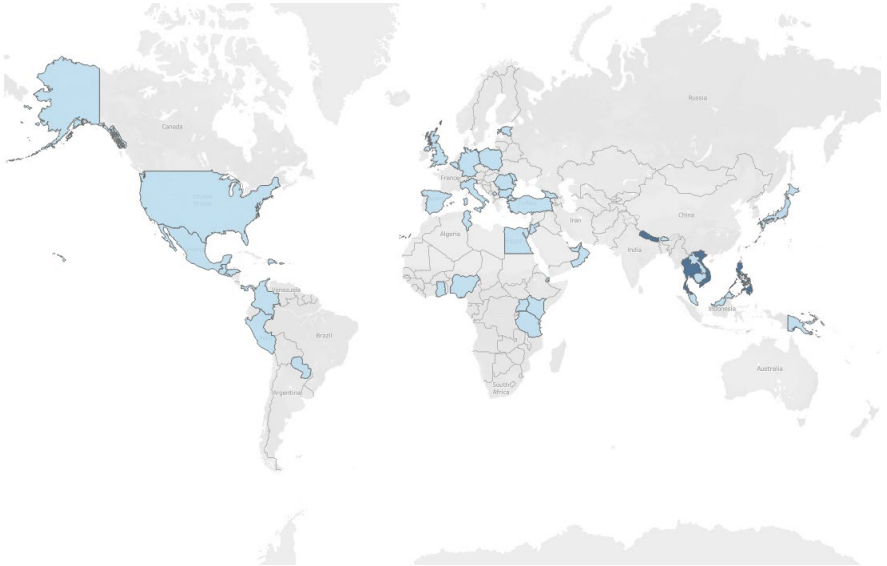
- **Comprehensive Epidemiology and Analysis Capabilities**
  - Over 12 million Active Component records (health care utilization, immunizations, deployment, reportable diseases, etc.)
    - ✓ Produce *Medical Surveillance Monthly Report* (*MSMR*), ad-hoc requests, studies/analyses
    - ✓ Weekly influenza reports
    - ✓ Vaccine safety and effectiveness studies

Influenza Surveillance in the DoW: GEIS

- The Global Emerging Infectious Surveillance (GEIS) partner laboratories form a wide-reaching network across the globe.

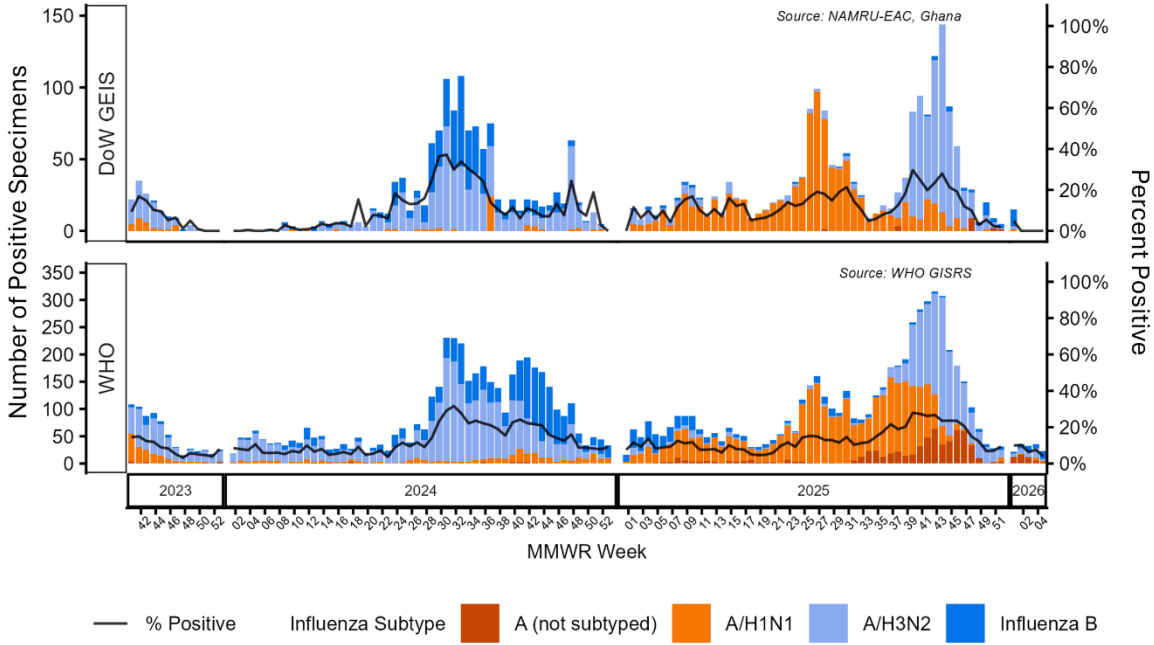
- Influenza surveillance activities in the DoW complement other existing global efforts:
  - Surveil some locations where data do not otherwise exist (e.g., Djibouti, Tanzania)
  - Surveil service members and their beneficiaries, U.S. civilians, and foreign national populations
  - The DoW service member population is highly vaccinated and widely distributed across the globe.

GEIS-Funded Laboratory Influenza Surveillance Footprint



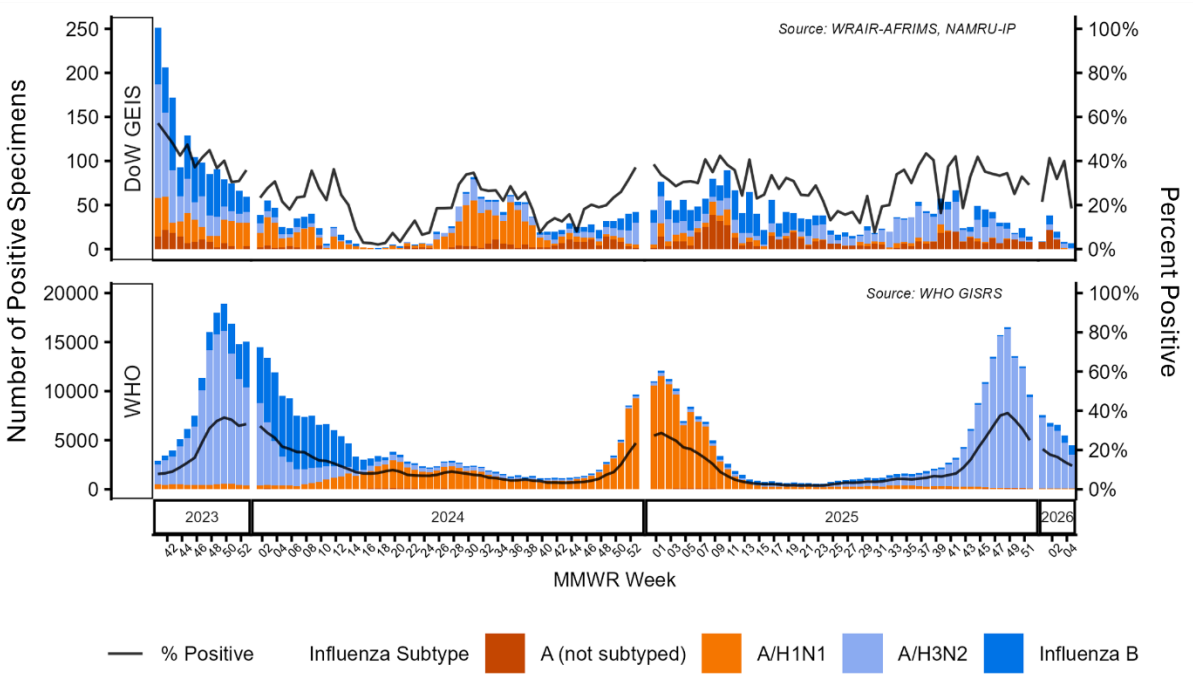
Influenza Surveillance: Subtype Circulation – West Africa

- Data collected from the GEIS surveillance network typically mirrors what is seen in WHO FluNet and in some cases may be the primary source of data.



Influenza Surveillance: Subtype Circulation – Asia

- Data collected from the GEIS surveillance network typically mirror what is seen in WHO FluNet and, in some cases, may be the primary source of data.
- Differences highlight the importance of using this surveillance stream to identify key samples for sequencing and advanced characterization.



DoW Influenza Mid-Season Vaccine Effectiveness (VE) (1)

Case-Control Study of DoW TRICARE Beneficiaries

Beneficiary VE: Study Design and Case Definition

- Adjusted Estimates of Vaccine Effectiveness
  - Population: DoW TRICARE beneficiaries, excluding service members
  - VE against medically-attended (outpatient), influenza-like illness (ILI), laboratory-confirmed influenza cases
  - Time period: November 9, 2025–February 21, 2026 (Weeks 46–07)

- Influenza-like illness case definition:
  - Fever (≥100.4°F) and cough, or
  - Fever (≥100.4°F) and two or more additional symptoms (fatigue, body aches, sore throat, headache, sinus congestion, shortness of breath, chills, runny nose, loss of taste or smell, nausea/vomiting/diarrhea, acute respiratory distress), or
  - Physician-diagnosed ILI

Beneficiary VE: Analyses

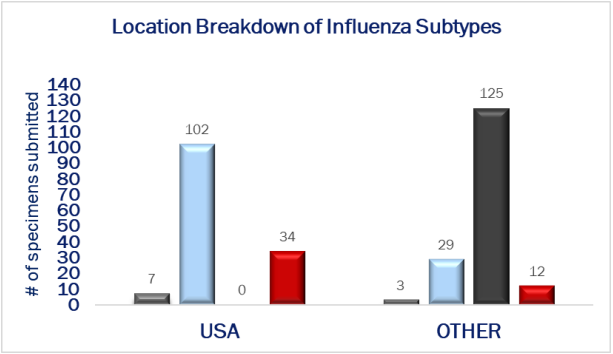
- Adjusted Estimates of Vaccine Effectiveness
  - Adjusted for age, month of illness, and region

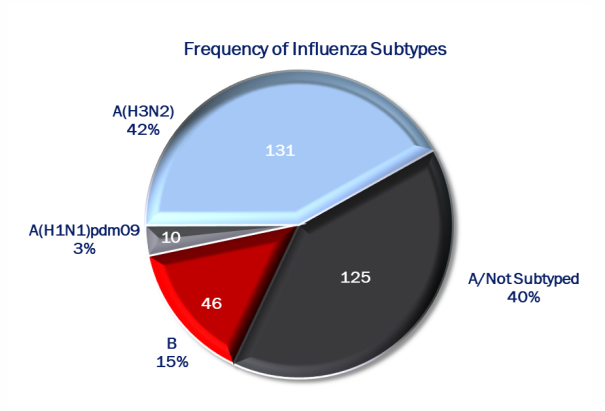
- Analyses by:
  - Influenza (overall) all dependents
  - Influenza (overall) adults (18–64 years)
  - Influenza (overall) children (6 months -17 years)
  - Influenza A (overall) all dependents
  - Influenza A (overall) adults (18-64 years)
  - Influenza A (overall) children (6 months -17 years)
  - Influenza A(H3N2) all dependents
  - Influenza A(H3N2) adults (18-64 years)
  - Influenza A(H3N2) children (6 months –17 years)
  - Influenza A (H1N1)pdm09 all dependents
  - Influenza B (overall) all dependents
  - Influenza B (overall) children (6 months -17 years)

Breakdown of Data for VE analyses

- Laboratories contributing to analyses:
  - DCPH-D: n=627 (62%)
  - Landstuhl Regional Medical Center (LRMC): n=377 (38%)

- Cases: n=312 (31%)
  - 211 (68%) vaccinated
  - 101 (32%) unvaccinated
- Controls: n=692 (69%)
  - 466 (67%) vaccinated
  - 226 (33%) unvaccinated





Beneficiary VE: Case/Control Characteristics

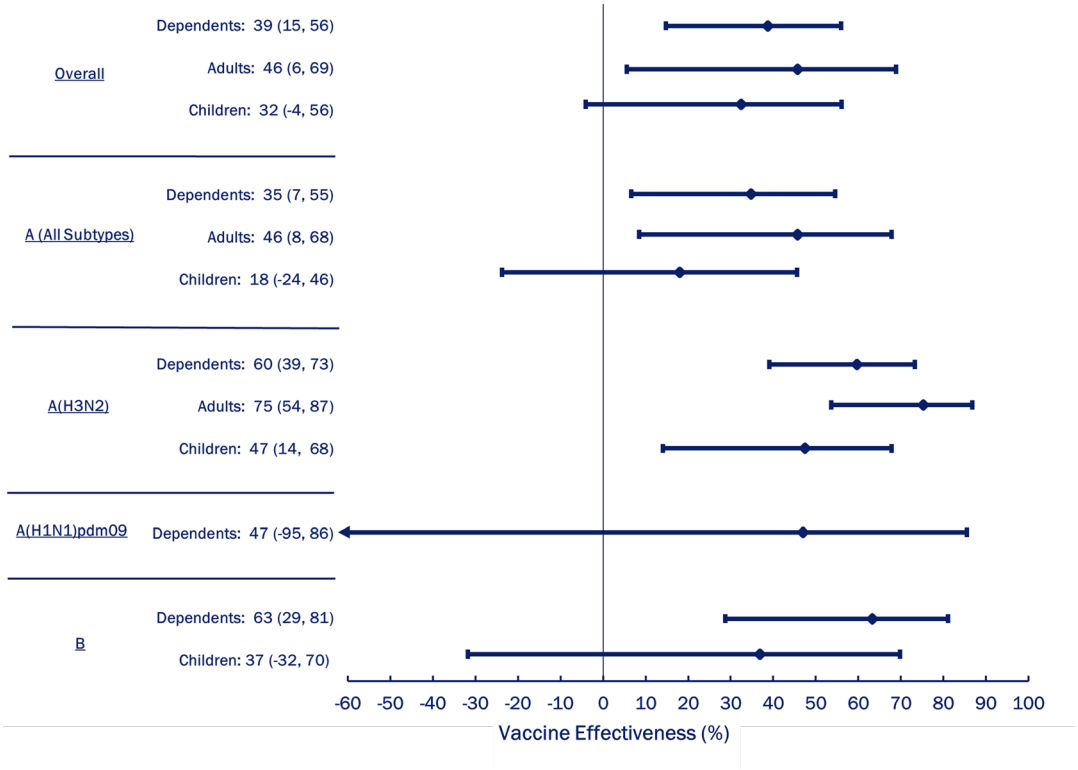
Characteristic		Cases n=312 No.(%)	Controls n=692 No.(%)	p-Value
Gender	Male	145 (46.5)	264 (38.2)	0.0130
	Female	167 (53.5)	428 (61.8)	
Age	6m-5	81 (26.0)	208 (30.1)	<0.0001
	6-9	51 (16.3)	66 (9.5)	
	10-17	93 (29.8)	116 (16.8)	
	18-24	18 (5.8)	37 (5.3)	
	25-44	43 (13.8)	159 (23.0)	
	45-64	26 (8.3)	106 (15.3)	
Beneficiary Category	Adult (18-64)	87 (27.9)	302 (43.6)	<0.0001
	Child (6m-17)	225 (72.1)	390 (56.4)	
Month of Illness	November	27 (8.6)	127 (18.4)	0.0002
	December	88 (28.2)	212 (30.6)	
	January	111 (35.6)	199 (28.8)	
	February	86 (27.6)	154 (22.2)	

Beneficiary VE: 2025-2026 Mid-Season Influenza Estimates (1 of 2)

Type	Population	Vaccine Status	Cases (%)	Controls (%)	Crude VE (95% CI)	Adjusted VE (95% CI)
Overall	Dependents	Yes	211 (21)	466 (46)	-1 (-35, 24)	39 (15, 56)
		No	101 (10)	226 (23)		
Overall	Adults	Yes	51 (13)	195 (50)	22 (-27, 52)	46 (6, 69)
		No	36 (9)	107 (28)		
Overall	Children	Yes	160 (26)	271 (44)	-8 (-55, 25)	32 (-4, 56)
		No	65 (11)	119 (19)		
A	Dependents	Yes	185 (19)	466 (49)	-11 (-50, 18)	35 (7, 55)
		No	81 (8)	226 (24)		
A	Adults	Yes	48 (6)	466 (60)	27 (-17, 55)	46 (8, 68)
		No	32 (4)	226 (29)		
A	Children	Yes	137 (16)	466 (53)	-36 (-95, 6)	18 (-24, 46)
		No	49 (6)	226 (26)		
A(H3N2)	Dependents	Yes	61 (7)	466 (57)	58 (38, 71)	60 (39, 73)
		No	70 (9)	226 (27)		
A(H3N2)	Adults	Yes	17 (2)	466 (63)	72 (47, 85)	75 (54, 87)
		No	29 (4)	226 (31)		
A(H3N2)	Children	Yes	44 (6)	466 (60)	48 (18, 67)	47 (14, 68)
		No	41 (5)	226 (29)		
A(H1N1)pdm09	Dependents	Yes	5 (1)	466 (66)	52 (-69, 86)	47 (-95, 86)
		No	5 (1)	226 (32)		
B	Dependents	Yes	26 (4)	466 (63)	37 (-15, 66)	63 (29, 81)
		No	20 (3)	226 (31)		
B	Children	Yes	23 (3)	466 (64)	30 (-35, 64)	37 (-32, 70)
		No	16 (2)	226 (31)		

- **Overall Influenza:** VE was low and significant, producing 39% effectiveness in all dependents. In adults, VE was moderate and significant at 46% and low and not significant in children at 32%.
- **Influenza A (all subtypes):** VE was higher among adults (46%) than in all dependents (35%) and significant. The children population produced lower estimates and was not significant at 18%.
- **A(H3N2):** VE was moderate to highly protective and significant among all dependents (60%), adults (75%) and children (47%)
- **A(H1N1)pdm09:** VE was moderately protective and not significant among all dependents (47%).
- **Influenza B:** VE was more effective in the dependent population at 63% and significant. In the children, it was effective at 37% but not significant.

Beneficiary VE: 2025-2026 Mid-Season Influenza Estimates (2 of 2)



- **Overall Influenza:** VE was low and significant, producing 39% effectiveness in all dependents. In adults, VE was moderate and significant at 46% and low and not significant in children at 32%.
- **Influenza A (all subtypes):** VE was higher among adults (46%) than in all dependents (35%) and significant. The children population produced lower estimates and was not significant at 18%.
- **A(H3N2):** VE was moderate to highly protective and significant among all dependents (60%), adults (75%) and children (47%)
- **A(H1N1)pdm09:** VE was moderately protective and not significant among all dependents (47%).
- **Influenza B:** VE was more effective in the dependent population at 63% and significant. In the children, it was effective at 37% but not significant.

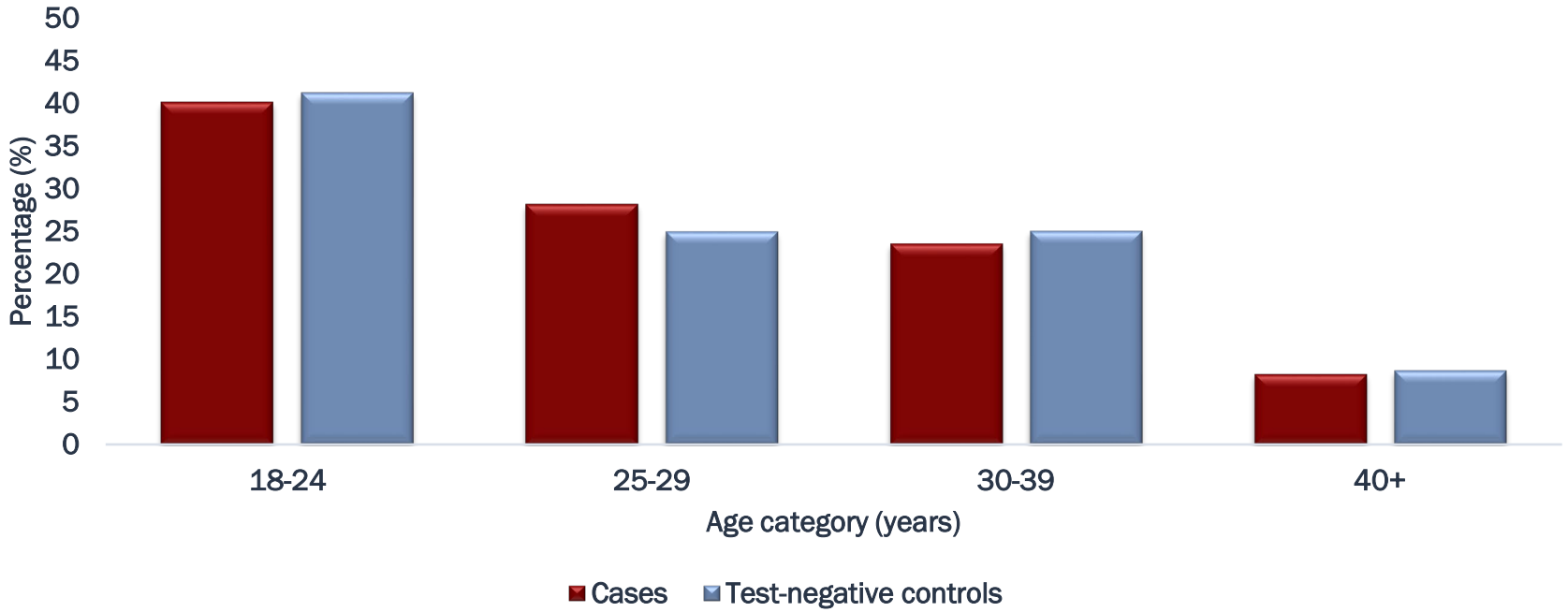
DoW Influenza Mid-Season Vaccine Effectiveness (2)

Case Test-Negative Control Design: Ambulatory Care
U.S. Active Component Service Members

U.S. Service Members VE: Study Design (Ambulatory)

- Case test-negative control design (ambulatory subjects only)
- Population: Active component service members
- Army, Navy, Air Force, Marine Corps, Coast Guard, and Space Force
- Time Period: December 1, 2025 – February 11, 2026
- Lab-confirmed flu cases: positive by rapid, RT-PCR, or culture assays
- Test-negative Controls: negative by RT-PCR or culture assays (subjects with negative rapid excluded)
- Models adjusted for sex, age category, prior vaccination (yes or no in previous 5 years), and month of diagnosis

U.S. Service Members VE: Age Breakdown (Ambulatory)



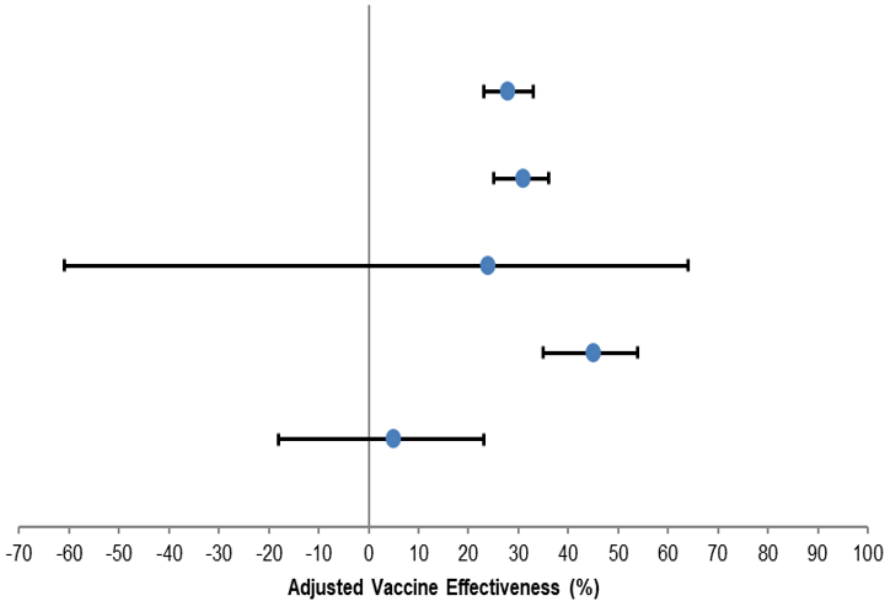
U.S. Service Members VE: Vaccination & Cases (Ambulatory)

- Vaccination
  - Vaccination types included inactivated (80%), cell-based (14%), and other (6%)
  - 79% of subjects had prior flu vaccine in previous 5 years
- Cases
  - Influenza A (any subtype) = 5,893
  - Influenza A(H3N2) = 747
  - Influenza A(H1N1)pdm09 = 51
  - Influenza B = 738

U.S. Service Members VE: Interim Estimates (Ambulatory)

Influenza Type	No. Cases (% Vaccinated)	No. Controls (% Vaccinated)	Crude VE (95% CI)	Adjusted VE (95% CI)*
Overall	6,611 (76)	19,033 (78)	8 (2, 14)	28 (23, 33)
A (All subtypes)	5,893 (75)	19,033 (78)	12 (6, 18)	31 (25, 36)
A(H1N1)pdm09	51 (82)	19,033 (78)	-35 (-277, 35)	24 (-61, 64)
A(H3N2)	747 (68)	19,033 (78)	38 (23, 47)	45 (35, 54)
B	738 (83)	19,033 (78)	-43 (-74, -17)	5 (-18, 23)

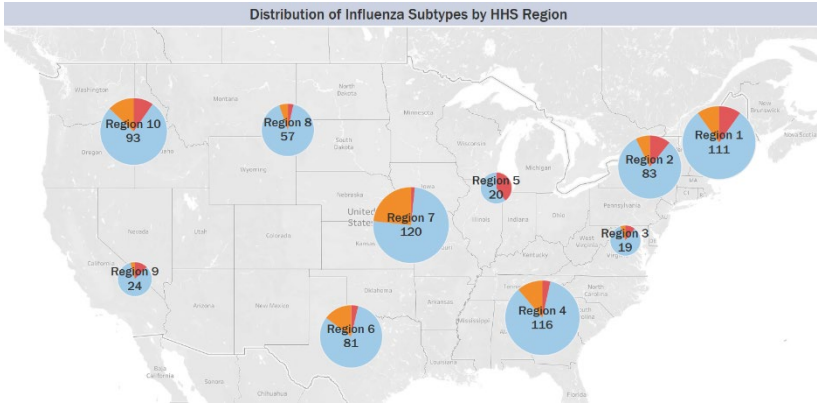
*Adjusted for sex, age category, 5-year prior vaccination (Y/N), and month of diagnosis

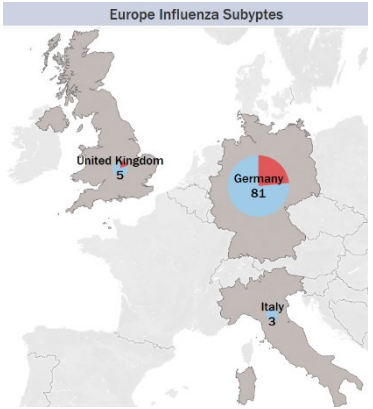


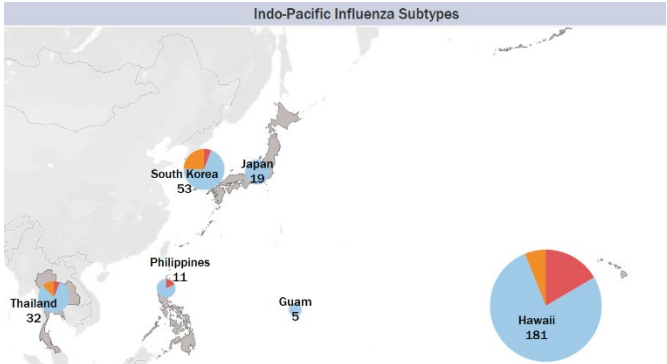
DoW Sequencing & Phylogenetic Analyses – Outline

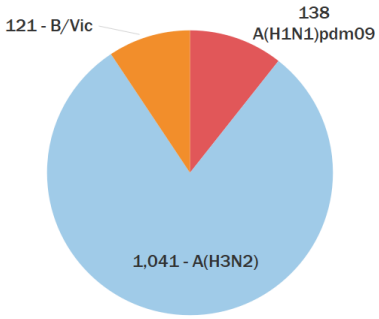
- Geographical distribution of influenza viruses characterized for the DoW
- Influenza A(H1N1)pdm09 phylogeny and cartography
- Influenza A(H3N2) phylogeny and cartography
- Influenza B subclade phylogeny and cartography

Geographical Distribution of 2025–2026 DoW Influenza Sequence Data

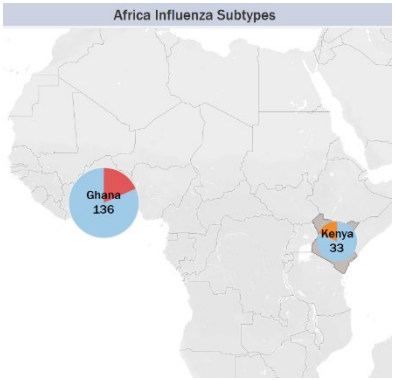




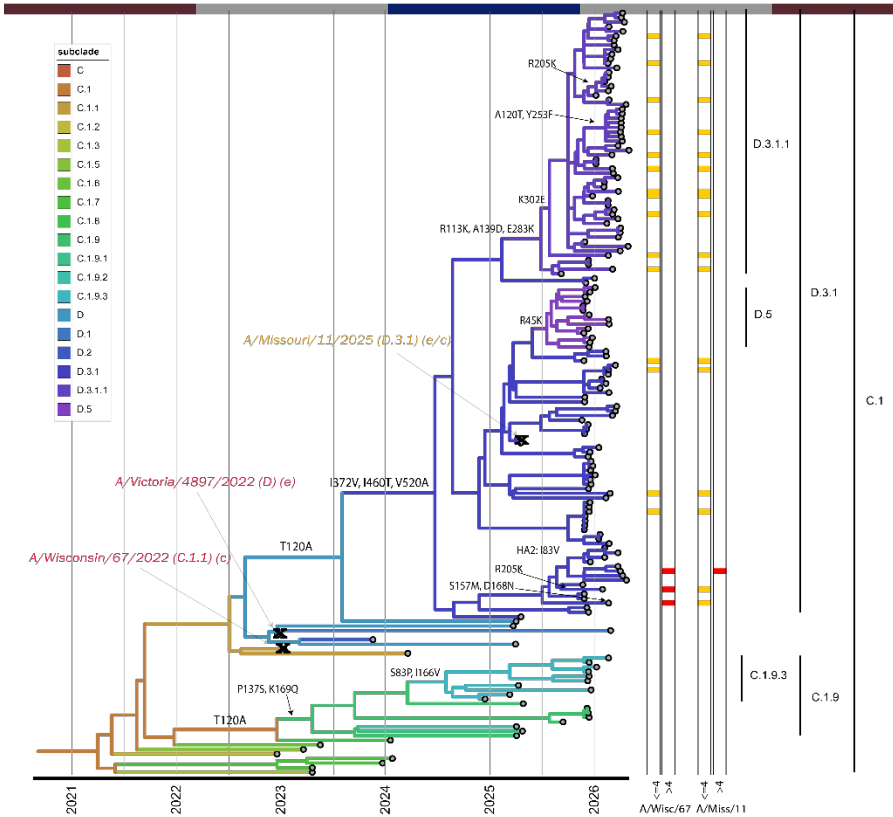




Overall: 1,300

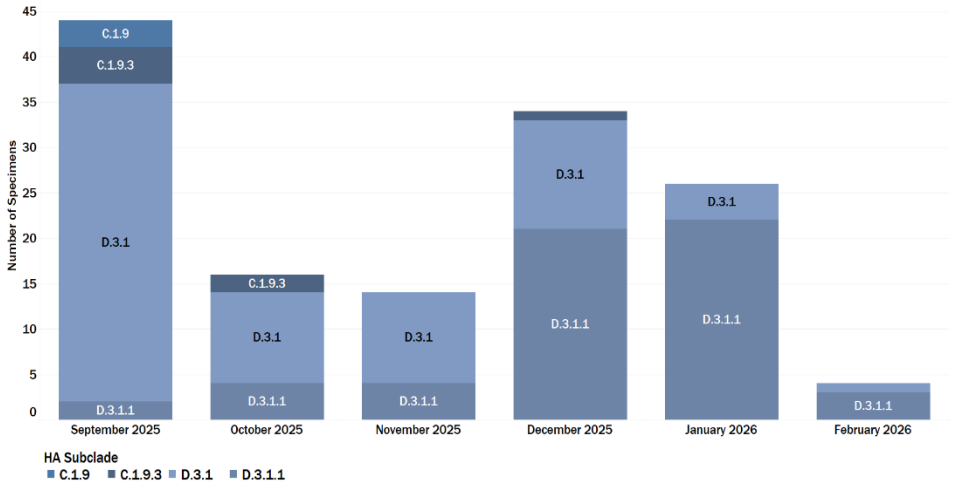


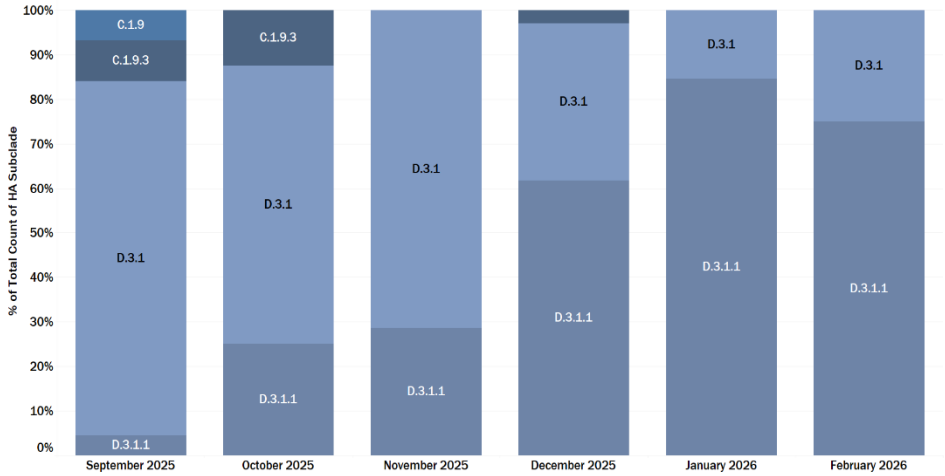
DoW Phylogenetic Analyses – A(H1N1)pdm09 HA



Clade/Subclade	No.	%
5a.2a	10	7.2%
C.1.9	3	30.0%
C.1.9.3	7	70.0%
5a.2a.1	128	92.8%
D.3.1	72	56.3%
D.3.1.1	56	43.7%

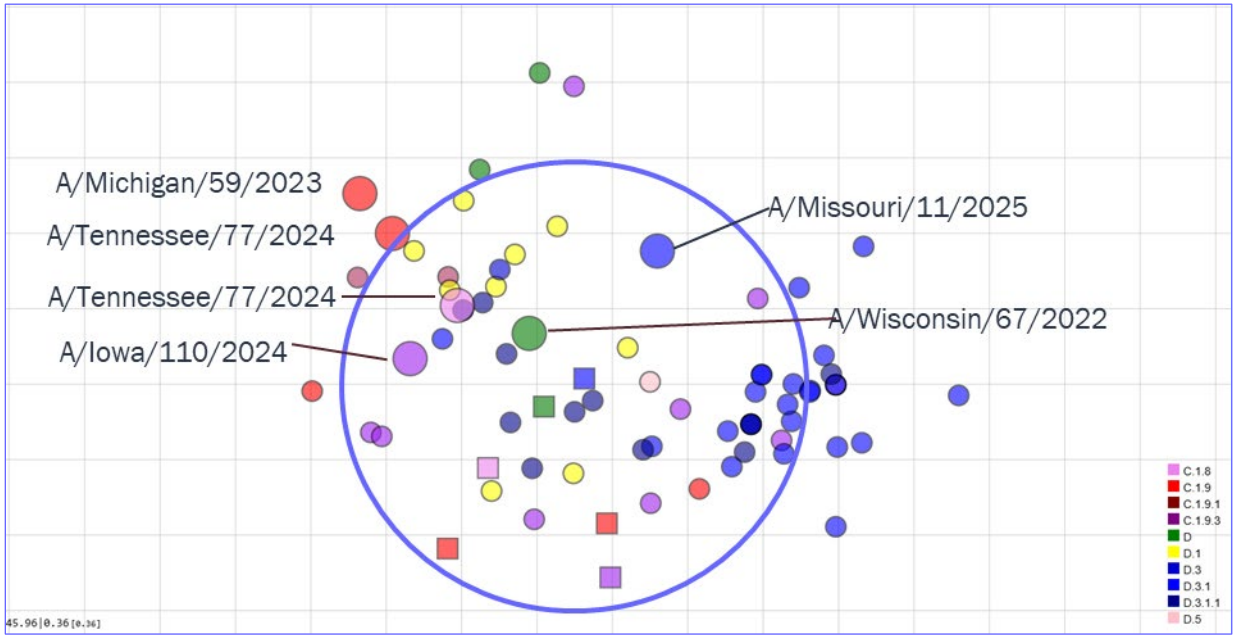
A(H1N1)pdm09 Clade Dynamics





- Proportionally, the season started with mostly D.3.1 followed by D.3.1.1
- Potentially, D.3.1 is beginning to increase in proportion as of February

DoW Antigenic Cartography: Influenza A/H1N1 isolates



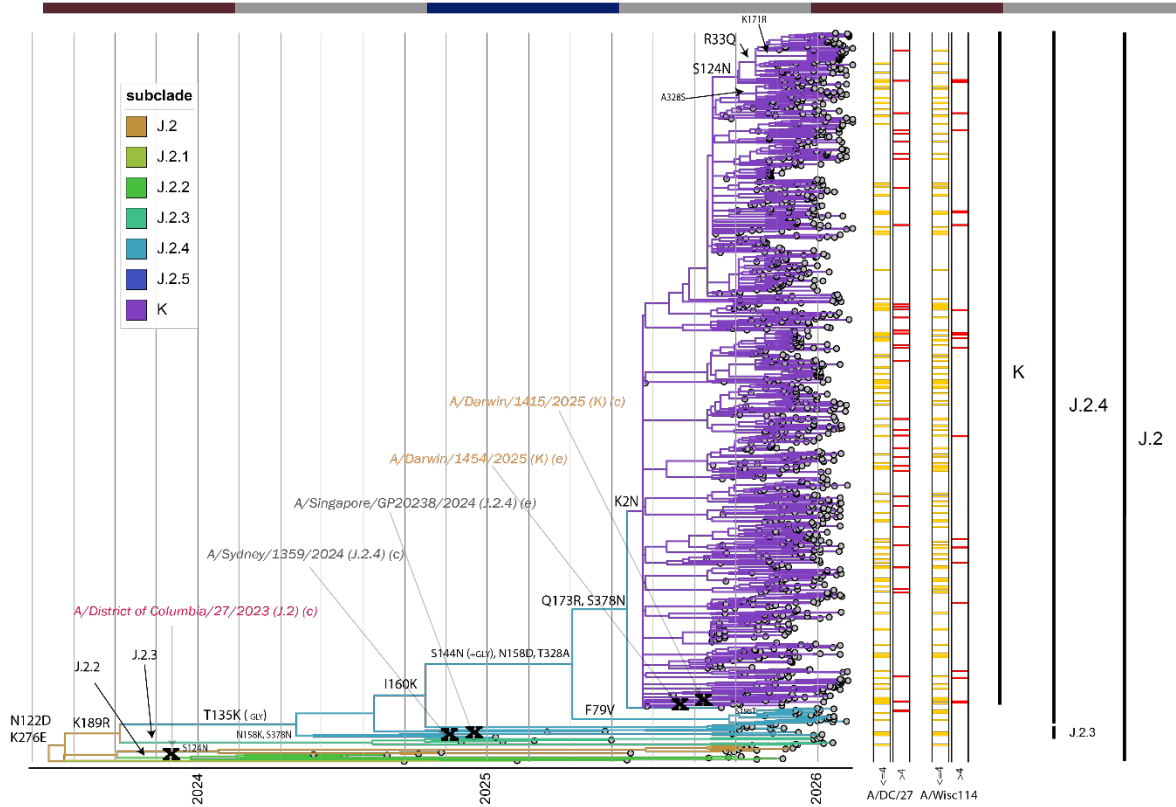
- Most circulating viruses are antigenically similar (<8-fold) to antisera to A/Missouri/11/20205.
- D.3.1.1 and particularly D.3.1 viruses are separating antigenically from A/Wisconsin/67/2022.

A(H1N1)pdm09 HINT Titer Table

			Reference Antisera						
			A/WI/67/22 c	A/Vic/4897/22 e	A/CT/17/23	A/MI/59/23	A/IA/110/24	A/MO/11/25 c	A/MO/11/25 e
		Clade	C.1.1	D	C.1.8	C.1.9	C.1.9.3	D.3.1	D.3.1
Reference Virus	A/Wisconsin/67/2022 c	C.1.1	**2560**	1280	1280	1280	640	1280	640
	A/Victoria/4897/2022 e	D	640	**320**	320	320	80	320	160
	A/Connecticut/17/2023	C.1.8	2560	640	**1280**	640	320	320	320
	A/Michigan/59/2023	C.1.9	320	160	320	**640**	160	320	320
	A/Iowa/110/2024	C.1.9.3	640	320	1280	1280	**640**	640	640
	A/Missouri/11/2025 c	D.3.1	640	640	640	320	320	**640**	1280
	A/Missouri/11/2025 e	D.3.1	10240	2560	5120	5120	1280	640	**640**
Test Virus	H125062	C.1.9	640	160	640	1280	160	160	80
	H125069	C.1.9	1280	640	1280	1280	1280	320	1280
	H125065	C.1.9.1	320	320	640	640	160	320	160
	H125066	C.1.9.1	640	320	1280	640	320	640	640
	H125073	C.1.9.3	1280	320	640	2560	1280	640	640
	H125092	C.1.9.3	640	320	320	640	640	320	640
	H125107	C.1.9.3	1280	2560	1280	1280	640	640	640
	H125063	D	640	320	320	320	80	320	320
	H125074	D	320	160	80	160	40	320	160
	H125081	D.1	1280	1280	640	1280	160	1280	320
	H125064	D.3.1	1280	640	640	320	160	640	320
	H125100	D.3.1	640	1280	320	320	640	640	640
	H125103	D.3.1	320	1280	160	160	320	320	640
	H125106	D.3.1	640	2560	320	640	1280	1280	2560
	H126002	D.3.1	640	1280	320	320	640	640	1280
	H126003	D.3.1.1	640	1280	640	320	1280	640	1280
	H126019	D.3.1.1	2560	2560	1280	2560	1280	2560	2560
	H126021	D.3.1.1	1280	1280	1280	1280	320	1280	1280
	H125070	D.5	1280	320	1280	1280	640	1280	1280
	H125095	D.5	320	320	160	160	320	320	1280

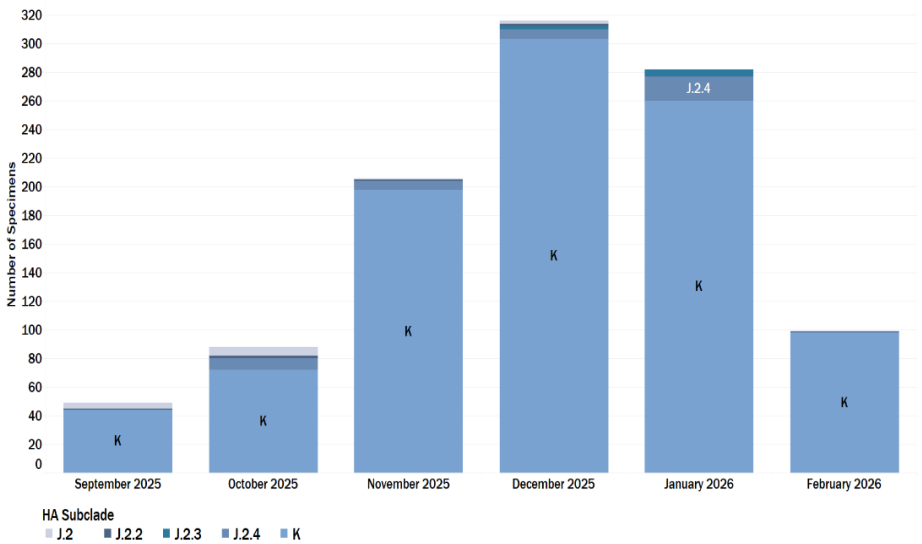
- Antisera to the subclade D.3.1 strain A/Missouri/11/2025 (egg and cell) slightly outperformed the 2025-2026 vaccine strains A/Wisconsin/67/2022 (cell) and A/Victoria/4897/2022 (egg) against D.3.1 and D.3.1.1 viruses by having more strains within an 8-fold range.

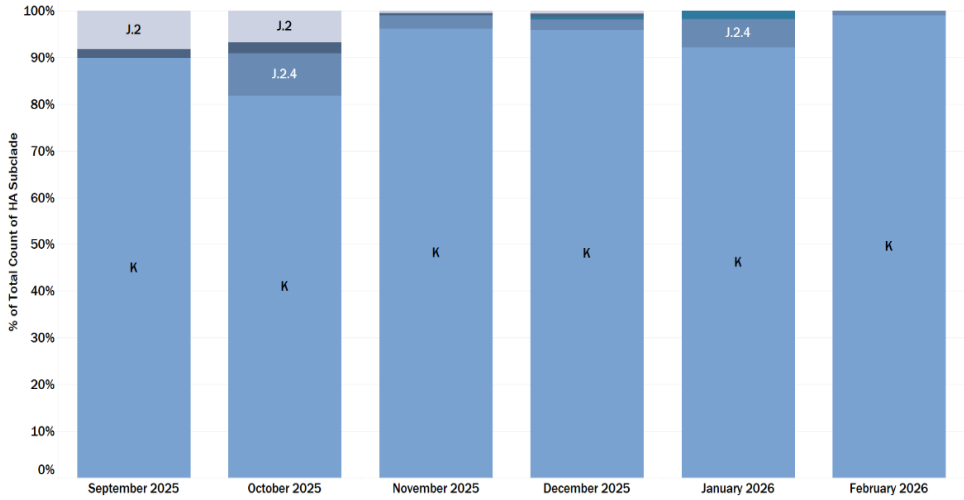
DoW Phylogenetic Analyses – A(H3N2) HA



Clade/Subclade	No.	%
2a.3a.1	1041	100%
J.2	14	1.3%
J.2.2	6	0.6%
J.2.3	7	0.7%
J.2.4	39	3.7%
K	975	93.7%

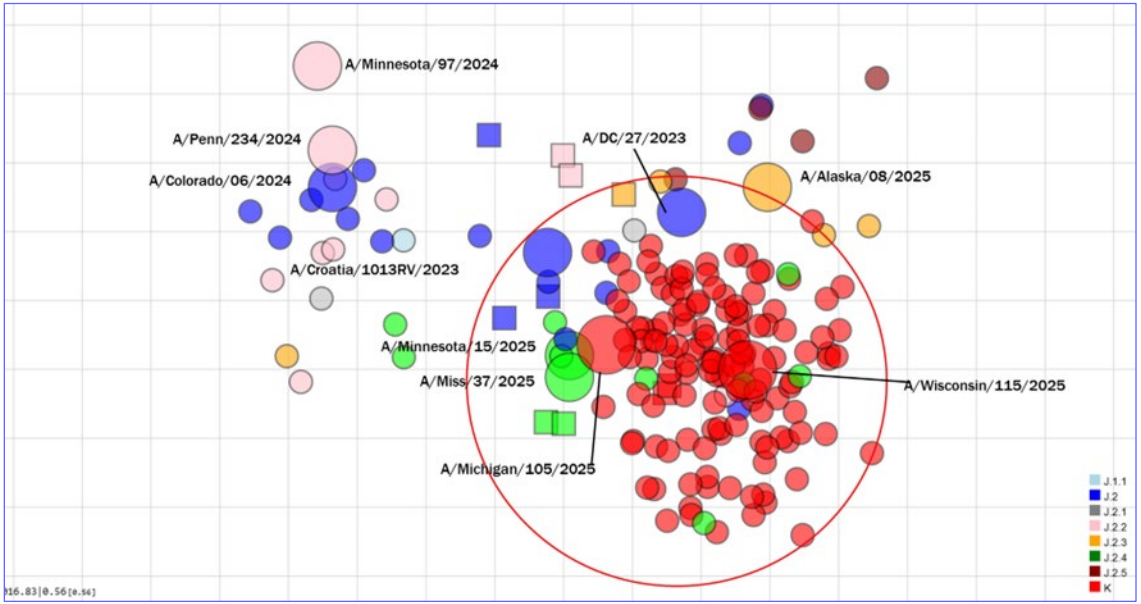
A(H3N2) Subclade Dynamics





- Subclade K has predominated throughout the season
- Other subclades such as J.2.3 and J.2.4 have still persisted in low numbers

DoW Antigenic Cartography: Influenza A/H3N2 Isolates



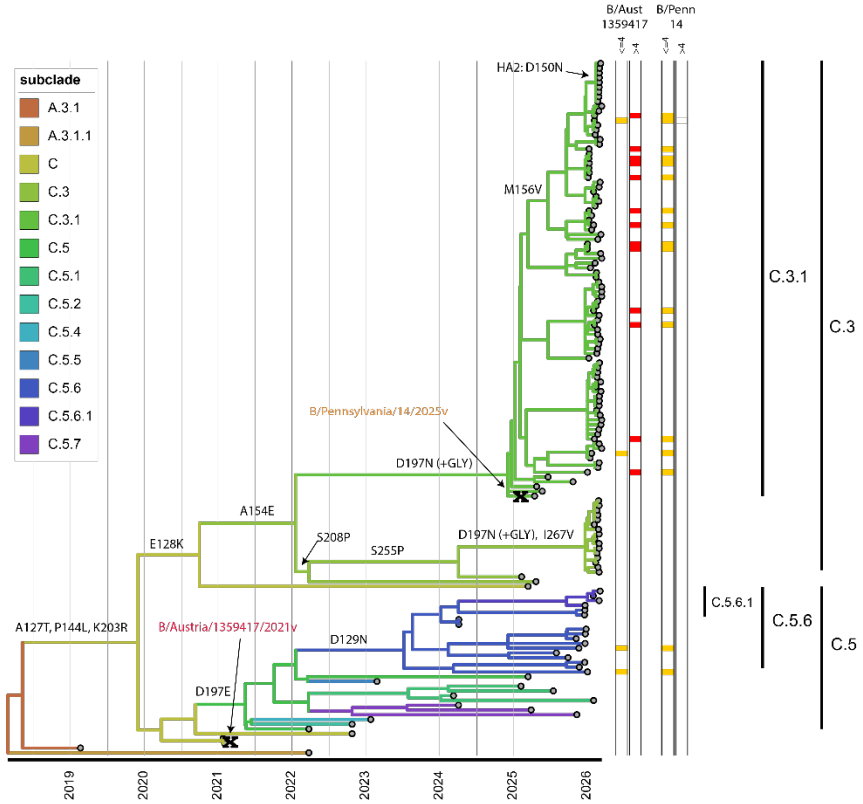
- Most subclade K viruses are antigenically distinct from other J.2 viruses.
- Subclade K viruses are well recognized by A/Michigan/105/2025, a A/Darwin/1415/2025-like virus.

A(H3N2) HINT Titer Table

			Reference Antisera							
			A/Cro/10136 RV/23 e	A/DC/27/23 c	A/CO/06/24	A/PA/234/24	A/AK/08/25	A/MN/15/25	A/MI/105/25 e	A/WI/114/25 c
		Clade	J.2	J.2	J.2.1	J.2.2	J.2.3	J.2.4	K	K
Reference Virus	A/DC/27/2023 c	J.2	**10240**	5120	2560	5120	2560	5120	5120	5120
	A/Croatia/10136RV/2023 e	J.2	5120	**1280**	640	1280	640	1280	2560	2560
	A/Colorado/06/2024	J.2.1	2560	640	**640**	320	320	640	320	320
	A/Pennsylvania/234/2024	J.2.2	1280	320	640	**320**	320	320	320	640
	A/Alaska/08/2025	J.2.3	1280	320	320	320	**1280**	1280	1280	1280
	A/Minnesota/15/2025	J.2.4	5120	2560	640	640	320	**5120**	10240	10240
	A/Michigan/105/2025	K	10240	2560	160	1280	1280	10240	**20480**	20480
	A/Wisconsin/114/2025	K	1280	320	80	320	640	2560	10240	**10240**
Test Virus	H325085	J.1.1	2560	640	320	1280	640	1280	1280	2560
	H325064	J.2	5120	1280	640	1280	1280	2560	2560	2560
	H325075	J.2	2560	640	80	160	640	5120	5120	5120
	H325103	J.2	2560	1280	640	640	640	1280	640	1280
	H325107	J.2	1280	640	640	640	320	640	640	640
	H325071	J.2.1	1280	640	640	320	80	1280	640	1280
	H325072	J.2.1	5120	640	640	2560	2560	2560	2560	5120
	H325066	J.2.2	1280	320	640	640	160	640	640	640
	H325086	J.2.2	1280	640	160	160	80	640	640	1280
	H325089	J.2.2	1280	320	160	160	160	320	320	1280
	H325104	J.2.2	2560	640	640	640	640	640	640	1280
	H325084	J.2.3	640	160	80	80	1280	1280	320	640
	H325088	J.2.3	1280	320	80	160	1280	1280	1280	1280
	H326082	J.2.3	2560	640	320	1280	2560	2560	1280	5120
	H326071	J.2.4	640	160	80	640	1280	2560	5120	2560
	H326088	J.2.4	2560	1280	80	320	640	2560	2560	2560
	H326128	J.2.4	1280	320	80	160	320	1280	5120	2560
	H326131	J.2.4	640	320	20	40	320	5120	5120	5120
	H325077	J.2.5	320	160	80	80	640	160	320	640
	H325079	J.2.5	2560	160	160	320	2560	640	640	640
	H325083	J.2.5	1280	160	160	160	2560	1280	640	640
	H325106	J.2.5	2560	1280	640	1280	2560	1280	1280	2560
	H325094	K	1280	320	320	640	2560	2560	5120	10240
	H325095	K	320	320	160	640	640	2560	5120	5120
	H326006	K	1280	640	80	640	640	5120	10240	10240
	H326117	K	640	640	80	160	320	640	1280	10240
	H326118	K	640	320	80	160	640	1280	5120	2560
	H326130	K	1280	640	160	640	1280	2560	10240	5120

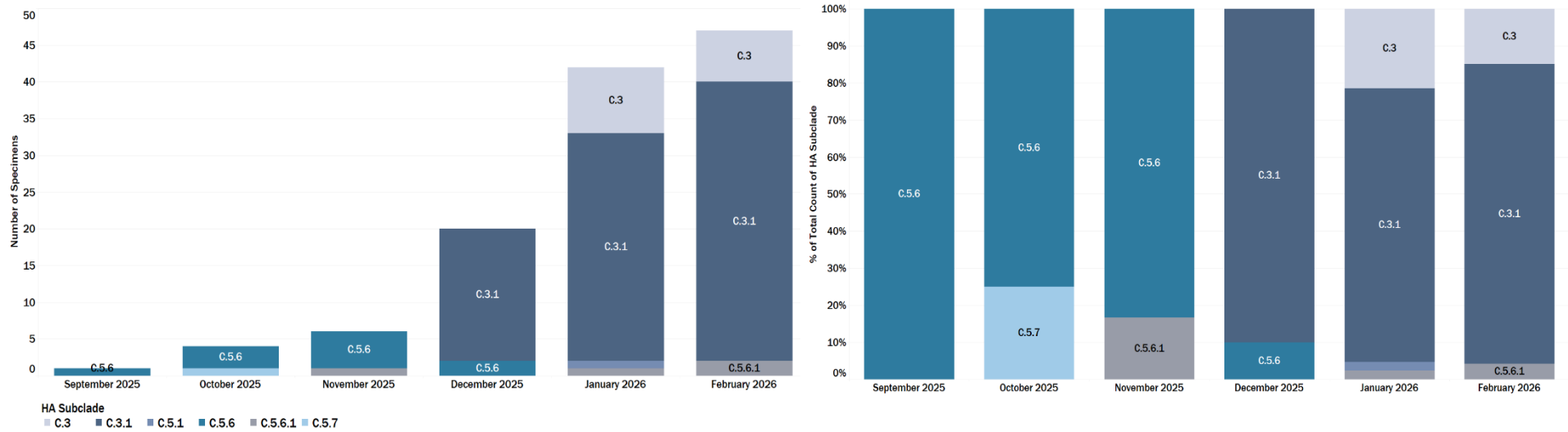
- Antisera to the subclade K strains A/Michigan/105/2025 (egg) and A/Wisconsin/114/2025 (cell) inhibited subclade K viruses much better than other antisera and generally provided protection across all subclades.
- A/Michigan/105/2025 and A/Wisconsin/114/2025 are A/Darwin/1454/2025-like and A/Darwin/1415/2025-like viruses, respectively.

DoW Phylogenetic Analyses – B/Victoria HA



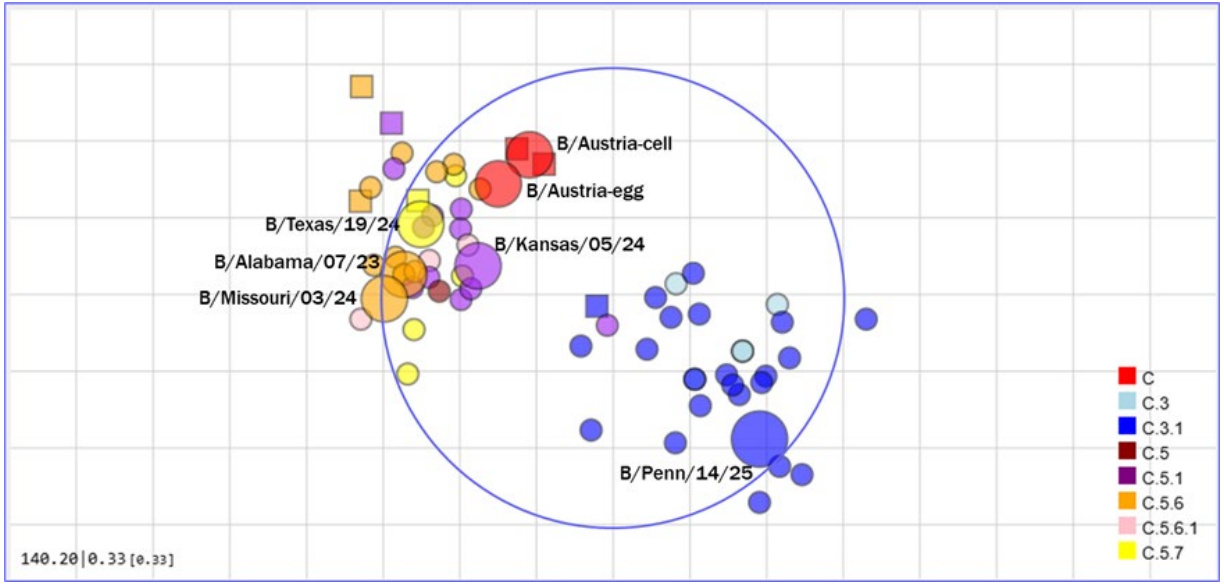
Clade/Subclade	No.	%
V1A.3a.2	121	100%
C.3	16	13.2%
C.3.1	87	71.9%
C.5.1	2	1.7%
C.5.6	11	9.1%
C.5.6.1	4	3.3%
C.5.7	1	0.8%

B/Vic Subclade Dynamics



- Subclade C.5.6 predominated early in the season but was replaced by C.3.1
- Other subclades such as C.3 and C.5.6.1 have still persisted in low numbers

DoW Antigenic Cartography: Influenza B isolates



- Subclade C.3.and C.3.1 viruses are antigenically separated from C and C.5 viruses.
- Subclade C.3 and C.3.1 viruses are well recognized by B/Pennsylvania/14/2025.

B/Victoria HINT Titer Table

			Reference Antisera					
			B/Aus/1359417/21 c	B/Aus/1359417/21 e	B/PA/14/25	B/KS/05/24	B/MO/03/24	B/TX/19/24
		Clade	C	C	C.3.1	C.5.1	C.5.6	C.5.7
Reference Virus	B/Austria/1359417/2021 c	C	**2560**	1280	640	2560	2560	2560
	B/Austria/1359417/2021 e	C	1280	**1280**	1280	5120	5120	2560
	B/Pennsylvania/14/2025	C.3.1	80	40	**640**	160	80	320
	B/Kansas/05/2024	C.5.1	640	320	1280	**5120**	2560	2560
	B/Missouri/03/2024	C.5.6	320	320	320	1280	**5120**	5120
	B/Texas/19/2024	C.5.7	640	320	640	5120	5120	**10240**
Test Virus	B25011	C.3	320	80	1280	160	320	640
	B25013	C.3	320	80	640	160	160	320
	B25016	C.3	320	320	1280	320	640	640
	B25017	C.3	320	80	1280	160	160	320
	B25027	C.3.1	160	80	1280	160	160	320
	B25036	C.3.1	160	160	1280	160	160	640
	B25048	C.3.1	320	80	640	80	160	320
	B26008	C.3.1	640	160	1280	640	320	640
	B26010	C.3.1	640	80	2560	640	640	640
	B25045	C.5	640	320	640	2560	5120	2560
	B25046	C.5.1	320	320	1280	5120	5120	5120
	B25047	C.5.1	320	320	640	2560	5120	5120
	B25020	C.5.1	640	640	1280	5120	5120	5120
	B25037	C.5.1	640	160	2560	640	640	2560
	B25010	C.5.6	640	320	320	2560	5120	5120
	B25014	C.5.6	640	320	320	2560	5120	5120
	B26003	C.5.6	640	320	320	2560	2560	5120
	B25033	C.5.6	1280	640	640	5120	5120	5120
	B25023	C.5.6.1	640	320	640	5120	5120	5120
	B25042	C.5.6.1	640	640	1280	2560	5120	5120
	B25009	C.5.7	320	160	640	1280	5120	5120
	B25030	C.5.7	320	160	320	1280	2560	2560
	B25008	C.5.7	640	320	1280	2560	5120	5120

- Antisera to the subclade C.3.1 strain B/Pennsylvania/14/2025 (cell) inhibited subclade C and C.3.1 viruses much better than other antisera, and still provided moderate protection again subclade C.5.1, C.5.6.1, and C.5.7 strains.

DoW Influenza Surveillance Summary (1)

- The DoW respiratory surveillance network maintains extensive global coverage and capabilities.
- Significant VE for DoW beneficiaries was highest among adults and dependents with A(H3N2) and dependents with B, and generally higher among adults in most flu types.
- Significant VE in active component population was moderate for A(H3N2) and low to moderate for overall and influenza A (all subtypes).
- RT-PCR data were contributed by DCPH-D, NAMRU-EAC (Ghana Det.), NAMRU-EAC (Cario Det.), NAMRU-IP, NHRC, NAMRU-S, WRAIR-Africa, LRMC, PHC-P, TAMC, WRAIR-EME, WRAIR-AFRIMS
- Sequence data were contributed by DCPH-D, LRMC, NAMRU-EAC (Ghana Det.), NAMRU-S, NHRC, PHC-P, TAMC, WRAIR-Africa, and WRAIR-AFRIMS.

DoW Influenza Surveillance Summary (2)

- 138 Influenza A(H1N1)pdm09 sequences were characterized: the dominant HA subclade was D.3.1 and the dominant NA clade was D.1 (data not shown). Circulating viruses are more closely related to A/Missouri/11/2025 than to A/Wisconsin/67/2022 and A/Victoria/4897/2022.
- 1,041 Influenza A(H3N2) sequences were characterized: the dominant HA subclade was K and the dominant NA clade was B.4.2.2 (data not shown). Circulating viruses are more closely related to A/Darwin/1415/2025-like and A/Darwin/1454/2025-like viruses than to A/District of Columbia/27/2023 and A/Croatia/10136RV/2023.
- 141 Influenza B/Victoria sequences were characterized: the dominant HA subclade was C.3.1 and the dominant NA clade was B.7.1 (data not shown). Circulating viruses are more closely related to B/Tokyo/EIS13-175/2025 and B/Pennsylvania/14/2025 than to B/Austria/1359417/2021.
- Our data agree with the WHO Northern Hemisphere influenza vaccine strain selections.

Questions?

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CDR Shayne Gallaway, PhD
Respiratory Focus Area Lead, Global Emerging Infections Surveillance Branch
Armed Forces Health Surveillance Division
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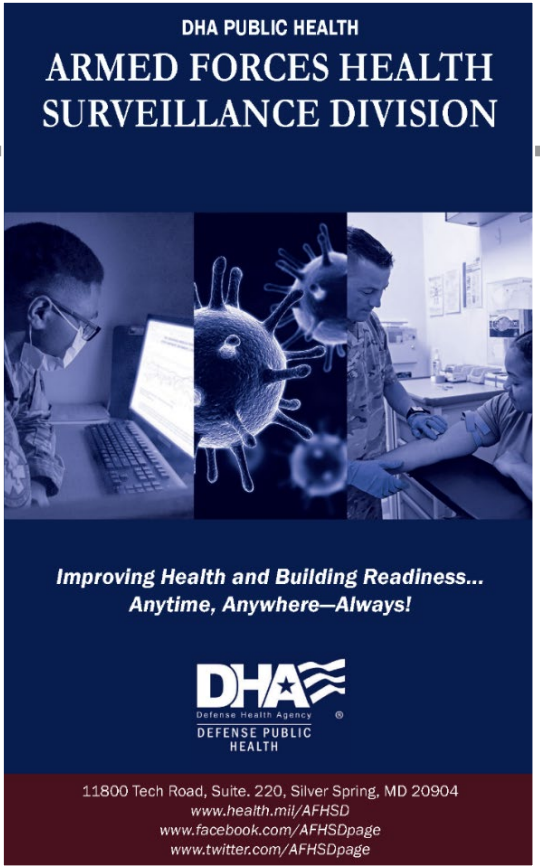
Questions?



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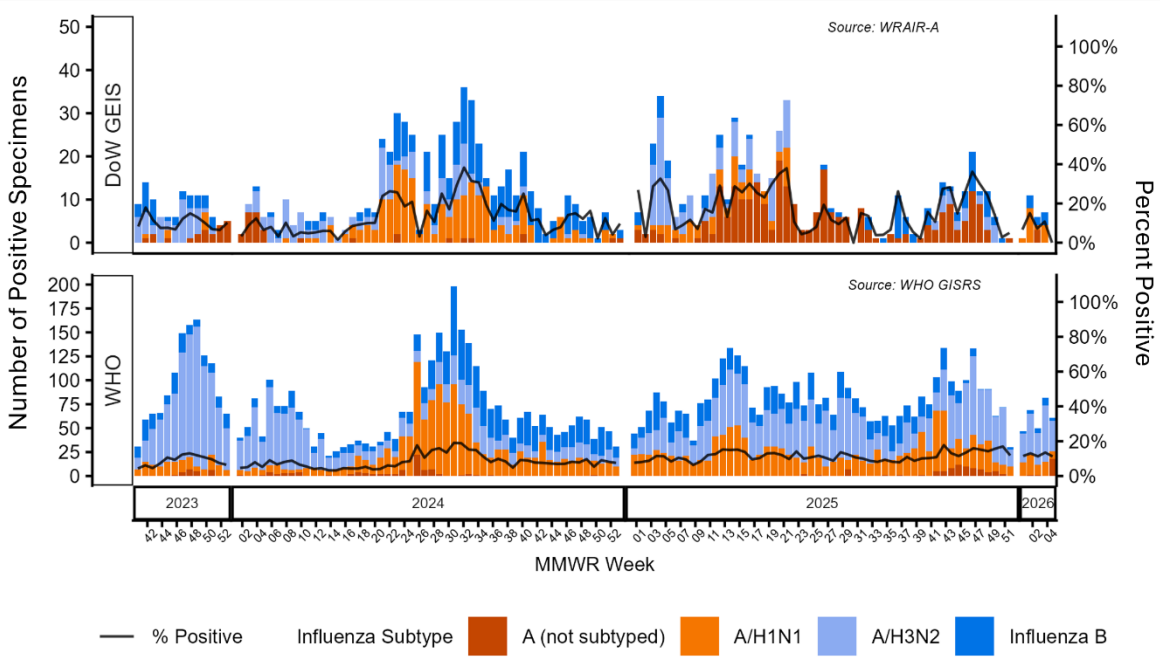
Back-up Slides

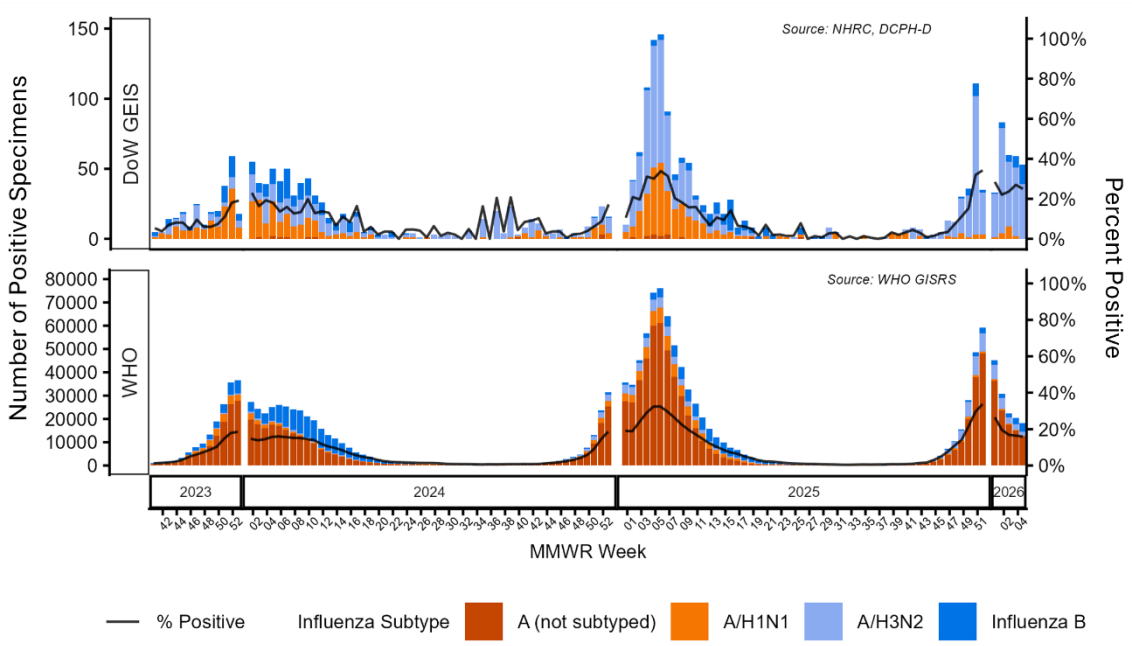
Influenza Surveillance: Subtype Circulation - East Africa

- Differences highlight the importance of using this surveillance stream to identify key samples for sequencing and advanced characterization.



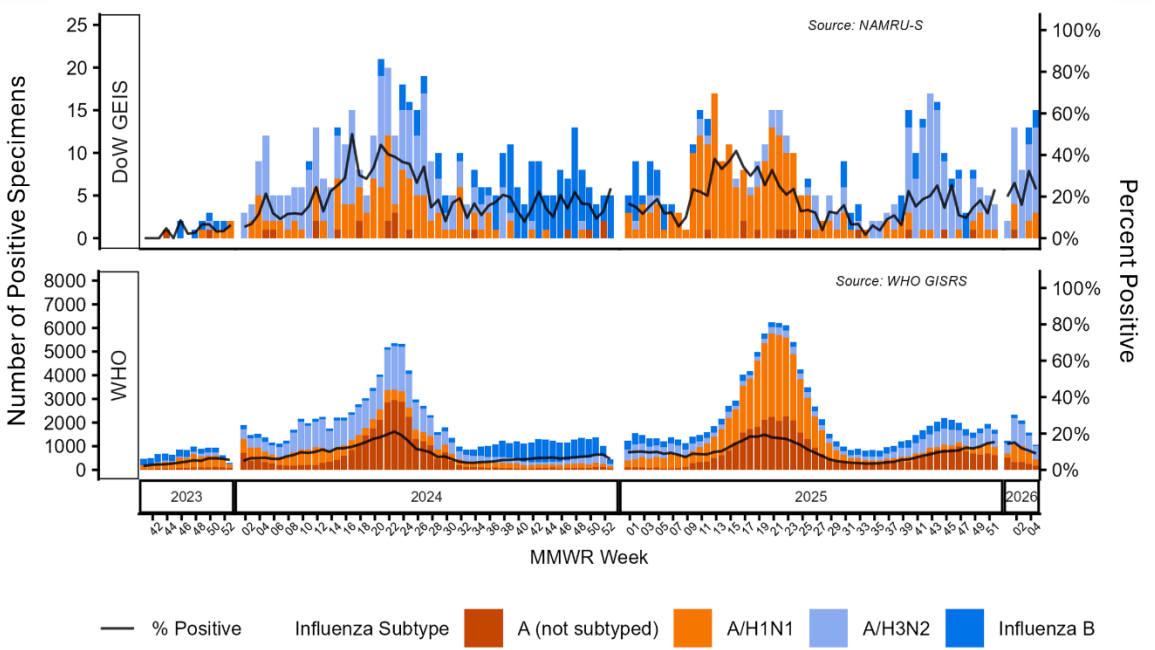
Influenza Surveillance: Subtype Circulation - North America

- Data collected from the GEIS surveillance network typically mirror what is seen in WHO FluNet and, in some cases, may be the primary source of data.
- Differences highlight the importance of using this surveillance stream to identify key samples for sequencing and advanced characterization.



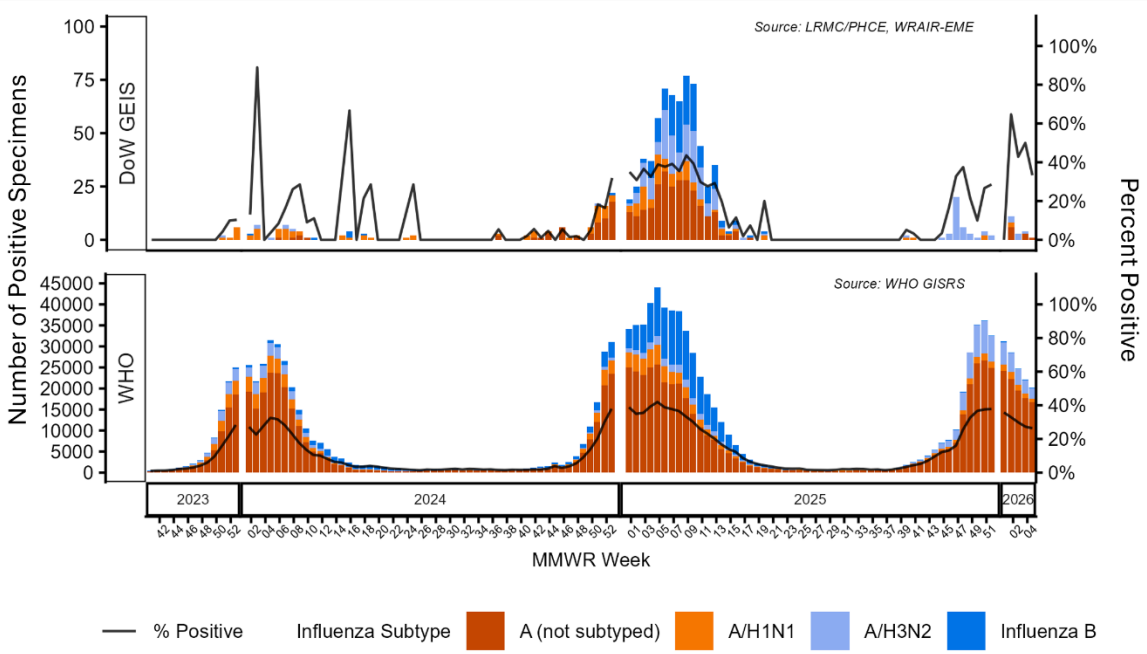
Influenza Surveillance: Subtype Circulation - South America

- Data collected from the GEIS surveillance network typically mirror what is seen in WHO FluNet and, in some cases, may be the primary source of data.
- Differences highlight the importance of using this surveillance stream to identify key samples for sequencing and advanced characterization.



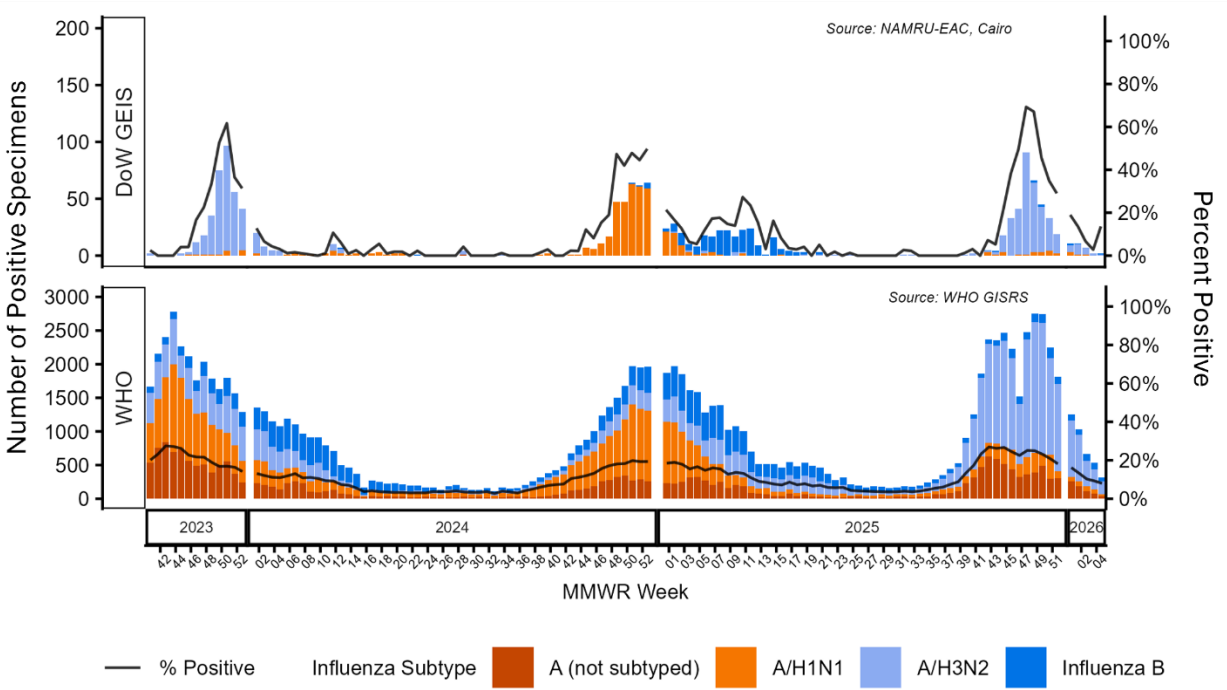
Influenza Surveillance: Subtype Circulation - Europe

- Data collected from the GEIS surveillance network typically mirror what is seen in WHO FluNet and, in some cases, may be the primary source of data.
- Differences highlight the importance of using this surveillance stream to identify key samples for sequencing and advanced characterization.



Influenza Surveillance: Subtype Circulation - Middle East

- Data collected from the GEIS surveillance network typically mirror what is seen in WHO FluNet and, in some cases, may be the primary source of data.
- Differences highlight the importance of using this surveillance stream to identify key samples for sequencing and advanced characterization.



Beneficiary VE: Case/Control Characteristics (2 of 2)

Characteristic		Cases n=312 No.(%)	Controls n=692 No.(%)	p-Value
Geographic Region	Eastern U.S.	52 (16.6)	140 (20.2)	0.0010
	Western U.S.	91 (29.2)	264 (38.2)	
	Other	169 (54.2)	288 (41.6)	
Vaccination Status	Vaccinated	211 (67.6)	466 (67.3)	0.9283
	Unvaccinated	101 (32.4)	226 (32.7)	
Influenza Status	Influenza A(H1N1)pdm09	10 (3.2)	0 (0)	<0.0001
	Influenza A(H3N2)	131 (42.0)	0 (0)	
	Influenza A/not subtyped	125 (40.1)	0 (0)	
	Influenza B	46 (14.7)	0 (0)	
	Not Influenza	0 (0)	692 (100)	